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RAW SEQUENCE LISTING

DATE: 03/19/2002

PATENT APPLICATION: US/10/007,132

TIME: 14:57:24

Input Set : N:\Crif3\RULE60\10007132.raw

Output Set: N:\CRF3\03192002\J007132.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Bard, Jonathan A

6 Borowsky, Beth

7 Smith, Kelli E

9 (ii) TITLE OF INVENTION: DNA ENCODING GALANIN GALR3 RECEPTORS
10 AND USES THEREOF

12 (iii) NUMBER OF SEQUENCES: 65

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Cooper & Dunham LLP

16 (B) STREET: 1185 Avenue of the Americas

17 (C) CITY: New York

18 (D) STATE: New York

19 (E) COUNTRY: U.S.A.

20 (F) ZIP: 10036

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk

24 (B) COMPUTER: IBM PC compatible

25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

28 (vi) CURRENT APPLICATION DATA:

C--> 29 (A) APPLICATION NUMBER: US/10/007,132

C--> 30 (B) FILING DATE: 03-Dec-2001

31 (C) CLASSIFICATION:

33 (vii) PRIOR APPLICATION DATA:

34 (A) APPLICATION NUMBER: 09/058,333

35 (B) FILING DATE:

38 (viii) ATTORNEY/AGENT INFORMATION:

39 (A) NAME: White, John P

40 (B) REGISTRATION NUMBER: 28,678

41 (C) REFERENCE/DOCKET NUMBER: 52241-E/JPW/KDB

43 (ix) TELECOMMUNICATION INFORMATION:

44 (A) TELEPHONE: 212 278 0400

45 (B) TELEFAX: 212 391 0525

48 (2) INFORMATION FOR SEQ ID NO: 1:

50 (i) SEQUENCE CHARACTERISTICS:

51 (A) LENGTH: 1280 base pairs

52 (B) TYPE: nucleic acid

53 (C) STRANDEDNESS: single

54 (D) TOPOLOGY: linear

W--> 56 (ii) MOLECULE TYPE: DNA

58 (ix) FEATURE:

59 (A) NAME/KEY: CDS

ENTERED

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60          (B) LOCATION: 63..1172
62          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
64 AGCTCCAGCC TAGGCGTTCT ACCTGGAAGA ATGCAGGGGC CCAGTACCTA GGACTGAGGA      60
66 AG ATG GCT GAC ATC CAG AAC ATT TCG CTG GAC AGC CCA GGG AGC GTA      107
67   Met Ala Asp Ile Gln Asn Ile Ser Leu Asp Ser Pro Gly Ser Val
68     1          5          10          15
70 GGG GCT GTG GCA GTG CCT GTG ATC TTT GCC CTC ATC TTC CTG TTG GGC      155
71 Gly Ala Val Ala Val Pro Val Ile Phe Ala Leu Ile Phe Leu Leu Gly
72     20          25          30
74 ATG GTG GGC AAT GGG CTG GTG TTG GCT GTG CTA CTG CAG CCT GGC CCA      203
75 Met Val Gly Asn Gly Leu Val Leu Ala Val Leu Leu Gln Pro Gly Pro
76     35          40          45
78 AGT GCC TGG CAG GAG CCA AGC AGT ACC ACA GAT CTC TTC ATC CTC AAC      251
79 Ser Ala Trp Gln Glu Pro Ser Ser Thr Thr Asp Leu Phe Ile Leu Asn
80     50          55          60
82 TTG GCC GTG GCC GAC CTT TGC TTC ATC CTG TGC TGC GTG CCC TTC CAG      299
83 Leu Ala Val Ala Asp Leu Cys Phe Ile Leu Cys Cys Val Pro Phe Gln
84     65          70          75
86 GCA GCC ATC TAC ACA CTG GAT GCC TGG CTC TTT GGG GCT TTC GTG TGC      347
87 Ala Ala Ile Tyr Thr Leu Asp Ala Trp Leu Phe Gly Ala Phe Val Cys
88     80          85          90          95
90 AAG ACG GTA CAT CTG CTC ATC TAC CTC ACC ATG TAT GCC AGC AGC TTC      395
91 Lys Thr Val His Leu Leu Ile Tyr Leu Thr Met Tyr Ala Ser Ser Phe
92     100         105         110
94 ACC CTG GCG GCC GTC TCC CTG GAC AGG TAC CTG GCT GTG CGG CAC CCA      443
95 Thr Leu Ala Ala Val Ser Leu Asp Arg Tyr Leu Ala Val Arg His Pro
96     115         120         125
98 CTG CGC TCC AGA GCC CTG CGC ACC CCG CGC AAC GCG CGC GCC GCC GTG      491
99 Leu Arg Ser Arg Ala Leu Arg Thr Pro Arg Asn Ala Arg Ala Ala Val
100    130         135         140
102 GGG CTC GTG TGG CTG CTG GCG GCT CTC TTT TCC GCG CCC TAC CTA AGC      539
103 Gly Leu Val Trp Leu Leu Ala Ala Leu Phe Ser Ala Pro Tyr Leu Ser
104    145         150         155
106 TAT TAC GGC ACG GTG CGC TAC GGC GCG CTC GAG CTC TGC GTG CCC GCT      587
107 Tyr Tyr Gly Thr Val Arg Tyr Gly Ala Leu Glu Leu Cys Val Pro Ala
108 160         165         170         175
110 TGG GAG GAC GCG CGG CGG CGC GCG CTG GAC GTG GCC ACC TTC GCC GCG      635
111 Trp Glu Asp Ala Arg Arg Arg Ala Leu Asp Val Ala Thr Phe Ala Ala
112    180         185         190
114 GGC TAC CTG CTG CCG GTG GCC GTG GTG AGC CTG GCC TAC GGA CGC ACG      683
115 Gly Tyr Leu Leu Pro Val Ala Val Val Ser Leu Ala Tyr Gly Arg Thr
116    195         200         205
118 CTA TGT TTC CTA TGG GCC GCC GTG GGT CCC GCG GGC GCG GCG GCA GCA      731
119 Leu Cys Phe Leu Trp Ala Ala Val Gly Pro Ala Gly Ala Ala Ala Ala
120    210         215         220
122 GAG GCG CGC AGA CGG GCG ACC GGC CGG GCG GGA CGC GCC ATG CTG GCA      779
123 Glu Ala Arg Arg Arg Ala Thr Gly Arg Ala Gly Arg Ala Met Leu Ala
124    225         230         235
126 GTG GCC GCG CTC TAC GCG CTT TGC TGG GGC CCG CAC CAC GCG CTC ATC      827

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127 Val Ala Ala Leu Tyr Ala Leu Cys Trp Gly Pro His His Ala Leu Ile
128 240                245                250                255
130 CTC TGC TTC TGG TAC GGC CGC TTC GCC TTC AGC CCG GCC ACC TAC GCC      875
131 Leu Cys Phe Trp Tyr Gly Arg Phe Ala Phe Ser Pro Ala Thr Tyr Ala
132                260                265                270
134 TGT CGC CTG GCC TCG CAC TGC CTC GCC TAC GCC AAC TCC TGC CTT AAC      923
135 Cys Arg Leu Ala Ser His Cys Leu Ala Tyr Ala Asn Ser Cys Leu Asn
136                275                280                285
138 CCG CTC GTC TAC TCG CTC GCC TCG CGC CAC TTC CGC GCG CGC TTC CGC      971
139 Pro Leu Val Tyr Ser Leu Ala Ser Arg His Phe Arg Ala Arg Phe Arg
140                290                295                300
142 CGC CTG TGG CCC TGC GGC CGT CGC CGC CAC CGC CAC CAC CAC CGC GCT      1019
143 Arg Leu Trp Pro Cys Gly Arg Arg Arg His Arg His His His Arg Ala
144                305                310                315
146 CAT CGA GCC CTC CGT CGT GTC CAG CCG GCG TCT TCG GGC CCC GCC GGT      1067
147 His Arg Ala Leu Arg Arg Val Gln Pro Ala Ser Ser Gly Pro Ala Gly
148 320                325                330                335
150 TAT CCC GGC GAC GCC AGG CCT CGT GGT TGG AGT ATG GAG CCC AGA GGG      1115
151 Tyr Pro Gly Asp Ala Arg Pro Arg Gly Trp Ser Met Glu Pro Arg Gly
152                340                345                350
154 GAT GCT CTG CGT GGT GGT GGA GAG ACT AGA CTA ACC CTG TCC CCC AGG      1163
155 Asp Ala Leu Arg Gly Gly Gly Glu Thr Arg Leu Thr Leu Ser Pro Arg
156                355                360                365
158 GGA CCT CAA TAACCCTGCC CGCTTGGACT CTGACGTCTG TCAGAATGCC      1212
159 Gly Pro Gln
160                370
162 ACCAAGGAAC ATCTAGGGAA CGGCAGTCTC GCCAGGCTCC ACCAAAAAGC AGAAGCAAAG      1272
164 TTGCAGGG      1280
167 (2) INFORMATION FOR SEQ ID NO: 2:
169     (i) SEQUENCE CHARACTERISTICS:
170         (A) LENGTH: 370 amino acids
171         (B) TYPE: amino acid
172         (D) TOPOLOGY: linear
174     (ii) MOLECULE TYPE: protein
176     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
178 Met Ala Asp Ile Gln Asn Ile Ser Leu Asp Ser Pro Gly Ser Val Gly
179 1      5      10      15
181 Ala Val Ala Val Pro Val Ile Phe Ala Leu Ile Phe Leu Leu Gly Met
182      20      25      30
184 Val Gly Asn Gly Leu Val Leu Ala Val Leu Leu Gln Pro Gly Pro Ser
185      35      40      45
187 Ala Trp Gln Glu Pro Ser Ser Thr Thr Asp Leu Phe Ile Leu Asn Leu
188      50      55      60
190 Ala Val Ala Asp Leu Cys Phe Ile Leu Cys Cys Val Pro Phe Gln Ala
191 65      70      75      80
193 Ala Ile Tyr Thr Leu Asp Ala Trp Leu Phe Gly Ala Phe Val Cys Lys
194      85      90      95
196 Thr Val His Leu Leu Ile Tyr Leu Thr Met Tyr Ala Ser Ser Phe Thr
197      100      105      110

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```

199 Leu Ala Ala Val Ser Leu Asp Arg Tyr Leu Ala Val Arg His Pro Leu
200      115      120      125
202 Arg Ser Arg Ala Leu Arg Thr Pro Arg Asn Ala Arg Ala Ala Val Gly
203      130      135      140
205 Leu Val Trp Leu Leu Ala Leu Phe Ser Ala Pro Tyr Leu Ser Tyr
206 145      150      155      160
208 Tyr Gly Thr Val Arg Tyr Gly Ala Leu Glu Leu Cys Val Pro Ala Trp
209      165      170      175
211 Glu Asp Ala Arg Arg Arg Ala Leu Asp Val Ala Thr Phe Ala Ala Gly
212      180      185      190
214 Tyr Leu Leu Pro Val Ala Val Val Ser Leu Ala Tyr Gly Arg Thr Leu
215      195      200      205
217 Cys Phe Leu Trp Ala Ala Val Gly Pro Ala Gly Ala Ala Ala Ala Glu
218      210      215      220
220 Ala Arg Arg Arg Ala Thr Gly Arg Ala Gly Arg Ala Met Leu Ala Val
221 225      230      235      240
223 Ala Ala Leu Tyr Ala Leu Cys Trp Gly Pro His His Ala Leu Ile Leu
224      245      250      255
226 Cys Phe Trp Tyr Gly Arg Phe Ala Phe Ser Pro Ala Thr Tyr Ala Cys
227      260      265      270
229 Arg Leu Ala Ser His Cys Leu Ala Tyr Ala Asn Ser Cys Leu Asn Pro
230      275      280      285
232 Leu Val Tyr Ser Leu Ala Ser Arg His Phe Arg Ala Arg Phe Arg Arg
233      290      295      300
235 Leu Trp Pro Cys Gly Arg Arg Arg His Arg His His Arg Ala His
236 305      310      315      320
238 Arg Ala Leu Arg Arg Val Gln Pro Ala Ser Ser Gly Pro Ala Gly Tyr
239      325      330      335
241 Pro Gly Asp Ala Arg Pro Arg Gly Trp Ser Met Glu Pro Arg Gly Asp
242      340      345      350
244 Ala Leu Arg Gly Gly Gly Glu Thr Arg Leu Thr Leu Ser Pro Arg Gly
245      355      360      365
247 Pro Gln
248      370
251 (2) INFORMATION FOR SEQ ID NO: 3:
253   (i) SEQUENCE CHARACTERISTICS:
254       (A) LENGTH: 1417 base pairs
255       (B) TYPE: nucleic acid
256       (C) STRANDEDNESS: single
257       (D) TOPOLOGY: linear
W--> 259   (ii) MOLECULE TYPE: DNA
261   (ix) FEATURE:
262       (A) NAME/KEY: CDS
263       (B) LOCATION: 1..1281
266   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
268 CAC TCA GCG ATG ACT TTG GCT CTG CTC TCC CCT CCT CCA TCT CCC ACG      48
269 His Ser Ala Met Thr Leu Ala Leu Leu Ser Pro Pro Pro Ser Pro Thr
W--> 270      375      380      385
272 AGC TTC CAG CCC AGA ACA CCT GGC CAG ACC CAG GTC GGG GGA GTT AGA      96

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	273	Ser	Phe	Gln	Pro	Arg	Thr	Pro	Gly	Gln	Thr	Gln	Val	Gly	Gly	Val	Arg	
W-->	274				390				395					400				
	276	TCC	CGG	GGT	CAA	GCA	ACC	AGA	ACT	GGG	GGC	TCT	TGC	CTG	AGG	ATT	CCA	144
	277	Ser	Arg	Gly	Gln	Ala	Thr	Arg	Thr	Gly	Gly	Ser	Cys	Leu	Arg	Ile	Pro	
W-->	278			405					410					415				
	280	GCT	TCT	CTT	CCC	AGG	TGC	CCG	TCT	GAT	GGG	GAG	ATG	GCT	GAT	GCC	CAG	192
	281	Ala	Ser	Leu	Pro	Arg	Cys	Pro	Ser	Asp	Gly	Glu	Met	Ala	Asp	Ala	Gln	
W-->	282			420					425					430				
	284	AAC	ATT	TCA	CTG	GAC	AGC	CCA	GGG	AGT	GTG	GGG	GCC	GTG	GCA	GTG	CCT	240
	285	Asn	Ile	Ser	Leu	Asp	Ser	Pro	Gly	Ser	Val	Gly	Ala	Val	Ala	Val	Pro	
W-->	286	435					440					445				450		
	288	GTG	GTC	TTT	GCC	CTA	ATC	TTC	CTG	CTG	GGC	ACA	GTG	GGC	AAT	GGG	CTG	288
	289	Val	Val	Phe	Ala	Leu	Ile	Phe	Leu	Leu	Gly	Thr	Val	Gly	Asn	Gly	Leu	
W-->	290				455						460					465		
	292	GTG	CTG	GCA	GTG	CTC	CTG	CAG	CCT	GGC	CCG	AGT	GCC	TGG	CAG	GAG	CCT	336
	293	Val	Leu	Ala	Val	Leu	Leu	Gln	Pro	Gly	Pro	Ser	Ala	Trp	Gln	Glu	Pro	
W-->	294				470					475				480				
	296	GGC	AGC	ACC	ACG	GAC	CTG	TTC	ATC	CTC	AAC	CTG	GCG	GTG	GCT	GAC	CTC	384
	297	Gly	Ser	Thr	Thr	Asp	Leu	Phe	Ile	Leu	Asn	Leu	Ala	Val	Ala	Asp	Leu	
W-->	298			485					490					495				
	300	TGC	TTC	ATC	CTG	TGC	TGC	GTG	CCC	TTC	CAG	GCC	ACC	ATC	TAC	ACG	CTG	432
	301	Cys	Phe	Ile	Leu	Cys	Cys	Val	Pro	Phe	Gln	Ala	Thr	Ile	Tyr	Thr	Leu	
W-->	302			500					505					510				
	304	GAT	GCC	TGG	CTC	TTT	GGG	GCC	CTC	GTC	TGC	AAG	GCC	GTG	CAC	CTG	CTC	480
	305	Asp	Ala	Trp	Leu	Phe	Gly	Ala	Leu	Val	Cys	Lys	Ala	Val	His	Leu	Leu	
W-->	306	515					520					525				530		
	308	ATC	TAC	CTC	ACC	ATG	TAC	GCC	AGC	AGC	TTT	ACG	CTG	GCT	GCT	GTC	TCC	528
	309	Ile	Tyr	Leu	Thr	Met	Tyr	Ala	Ser	Ser	Phe	Thr	Leu	Ala	Ala	Val	Ser	
W-->	310				535						540					545		
	312	GTG	GAC	AGG	TAC	CTG	GCC	GTG	CGG	CAC	CCG	CTG	CGC	TCG	CGC	GCC	CTG	576
	313	Val	Asp	Arg	Tyr	Leu	Ala	Val	Arg	His	Pro	Leu	Arg	Ser	Arg	Ala	Leu	
W-->	314				550						555					560		
	316	CGC	ACG	CCG	CGT	AAC	GCC	CGC	GCC	GCA	GTG	GGG	CTG	GTG	TGG	CTG	CTG	624
	317	Arg	Thr	Pro	Arg	Asn	Ala	Arg	Ala	Ala	Val	Gly	Leu	Val	Trp	Leu	Leu	
W-->	318				565						570				575			
	320	GCG	GCG	CTC	TTC	TCG	GCG	CCC	TAC	CTC	AGC	TAC	TAC	GGC	ACC	GTG	CGC	672
	321	Ala	Ala	Leu	Phe	Ser	Ala	Pro	Tyr	Leu	Ser	Tyr	Tyr	Gly	Thr	Val	Arg	
W-->	322			580					585					590				
	324	TAC	GGC	GCG	CTG	GAG	CTC	TGC	GTG	CCC	GCC	TGG	GAG	GAC	GCG	CGC	CGC	720
	325	Tyr	Gly	Ala	Leu	Glu	Leu	Cys	Val	Pro	Ala	Trp	Glu	Asp	Ala	Arg	Arg	
W-->	326	595					600					605				610		
	328	CGC	GCC	CTG	GAC	GTG	GCC	ACC	TTC	GCT	GCC	GGC	TAC	CTG	CTG	CCC	GTG	768
	329	Arg	Ala	Leu	Asp	Val	Ala	Thr	Phe	Ala	Ala	Gly	Tyr	Leu	Leu	Pro	Val	
W-->	330				615						620					625		
	332	GCT	GTG	GTG	AGC	CTG	GCC	TAC	GGG	CGC	ACG	CTG	CGC	TTC	CTG	TGG	GCC	816
	333	Ala	Val	Val	Ser	Leu	Ala	Tyr	Gly	Arg	Thr	Leu	Arg	Phe	Leu	Trp	Ala	
W-->	334				630						635				640			
	336	GCC	GTG	GGT	CCC	GCG	GGC	GCG	GCG	GCG	GCG	GAG	GCG	CGG	CGG	AGG	GCG	864
	337	Ala	Val	Gly	Pro	Ala	Gly	Ala	Ala	Ala	Ala	Glu	Ala	Arg	Arg	Arg	Ala	

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10007132.raw

Output Set: N:\CRF3\03192002\J007132.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:56 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1
L:259 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3
L:270 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:274 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:278 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:282 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:286 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:290 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:294 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:298 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:302 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:306 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:310 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:314 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:318 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:322 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:326 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:330 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:334 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:338 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:342 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:346 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:350 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:354 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:358 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:362 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:366 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:370 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:374 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:482 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5
L:561 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6
L:576 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7
L:591 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8
L:608 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9
L:623 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=10
L:638 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=11
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L:668 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=13
L:683 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=14
L:698 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=15
L:713 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=16
L:728 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=17
L:743 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=18
L:759 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=19
L:774 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=20
L:789 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=21

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Input Set : N:\Crf3\RULE60\10007132.raw

Output Set: N:\CRF3\03192002\J007132.raw

L:807 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=22
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L:852 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=25
L:867 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=26
L:882 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=27
L:897 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=28
L:912 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=29
L:927 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=30
L:942 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=31
L:957 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=32
L:972 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=33
L:987 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=34
L:1002 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=35
L:1017 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=36
L:1032 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=37
L:1047 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=38
L:1061 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=39
L:1076 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=40
L:1091 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=41
L:1106 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=42
L:1121 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=43
L:1136 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=44
L:1151 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=45
L:1166 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=46
L:1181 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=47
L:1199 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=48
L:1214 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=49
L:1229 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=50
L:1244 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=51
L:1258 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=52